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1635

TECH CENTER 1600/2900

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/603,124B

DATE: 04/26/2001

TIME: 13:10:35

Input Set : D:\seqlistcorrected2.txt

Output Set: N:\CRF3\04262001\I603124B.raw

#9/K.T.
5/4
Raw
ENTERED
seq.
see p.5 listing
(entered)

3 <110> APPLICANT: Pompejus, Markus
4 Kroger, Burkhard
5 Schroder, Hartwig
6 Zelder, Oskar
7 Haberhauer, Gregor
9 <120> TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
10 INVOLVED IN HOMEOSTASIS AND ADAPTATION
12 <130> FILE REFERENCE: BGI-132CP
14 <140> CURRENT APPLICATION NUMBER: 09/603124B
15 <141> CURRENT FILING DATE: 2000-06-23
17 <150> PRIOR APPLICATION NUMBER: US 60/141031
18 <151> PRIOR FILING DATE: 1999-06-25
20 <150> PRIOR APPLICATION NUMBER: US 60/143694
21 <151> PRIOR FILING DATE: 1999-07-14
23 <150> PRIOR APPLICATION NUMBER: US 60/151778
24 <151> PRIOR FILING DATE: 1999-08-31
26 <150> PRIOR APPLICATION NUMBER: DE 19931418.7
27 <151> PRIOR FILING DATE: 1999-07-08
29 <150> PRIOR APPLICATION NUMBER: DE 19932124.8
30 <151> PRIOR FILING DATE: 1999-07-09
32 <150> PRIOR APPLICATION NUMBER: DE 19932126.4
33 <151> PRIOR FILING DATE: 1999-07-09
35 <150> PRIOR APPLICATION NUMBER: DE 19932127.2
36 <151> PRIOR FILING DATE: 1999-07-09
38 <150> PRIOR APPLICATION NUMBER: DE 19932133.7
39 <151> PRIOR FILING DATE: 1999-07-09
41 <150> PRIOR APPLICATION NUMBER: DE 19932207.4
42 <151> PRIOR FILING DATE: 1999-07-09
44 <150> PRIOR APPLICATION NUMBER: DE 19932208.2
45 <151> PRIOR FILING DATE: 1999-07-09
47 <150> PRIOR APPLICATION NUMBER: DE 19932225.2
48 <151> PRIOR FILING DATE: 1999-07-09
50 <150> PRIOR APPLICATION NUMBER: DE 19932229.5
51 <151> PRIOR FILING DATE: 1999-07-09
53 <150> PRIOR APPLICATION NUMBER: DE 19932914.1
54 <151> PRIOR FILING DATE: 1999-07-14
56 <150> PRIOR APPLICATION NUMBER: DE 19933006.9
57 <151> PRIOR FILING DATE: 1999-07-14
59 <150> PRIOR APPLICATION NUMBER: DE 19940765.7
60 <151> PRIOR FILING DATE: 1999-08-27
62 <150> PRIOR APPLICATION NUMBER: DE 19940768.1
63 <151> PRIOR FILING DATE: 1999-08-27
65 <150> PRIOR APPLICATION NUMBER: DE 19940831.9
66 <151> PRIOR FILING DATE: 1999-08-27
68 <150> PRIOR APPLICATION NUMBER: DE 19940832.7
69 <151> PRIOR FILING DATE: 1999-08-27
71 <150> PRIOR APPLICATION NUMBER: DE 19941385.1

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72 <151> PRIOR FILING DATE: 1999-08-31
74 <150> PRIOR APPLICATION NUMBER: DE 19941396.7
75 <151> PRIOR FILING DATE: 1999-08-31
77 <150> PRIOR APPLICATION NUMBER: DE 19942087.4
78 <151> PRIOR FILING DATE: 1999-09-03
80 <160> NUMBER OF SEQ ID NOS: 480
82 <210> SEQ ID NO: 1
83 <211> LENGTH: 1581
84 <212> TYPE: DNA
85 <213> ORGANISM: Corynebacterium glutamicum
87 <220> FEATURE:
88 <221> NAME/KEY: CDS
89 <222> LOCATION: (101)..(1558)
90 <223> OTHER INFORMATION: RXA02702
92 <400> SEQUENCE: 1
93 gcaggtaacg cctccacggt gattgcagac atgattgctg caactatcaa tagccaacac 60
95 aactaaaacg accagctcaa cgcaaaggaa tagtttaag'gtg acc act cca cac 115
96                                     Val Thr Thr Pro His
97                                     1           5
99 ttg gat tct gca caa gat att gat ctg tcc cgc gtc cac ctc atc ggt 163
100 Leu Asp Ser Ala Gln Asp Ile Asp Leu Ser Arg Val His Leu Ile Gly
101             10             15             20
103 att ggc gga gcc gga atg tct ggc gtt gcc cga atc ctg ctt gcc cgc 211
104 Ile Gly Gly Ala Gly Met Ser Gly Val Ala Arg Ile Leu Leu Ala Arg
105             25             30             35
107 ggt aag aca gtc act ggt tcc gat gcc aaa gat tcc cgc acc ttg ctt 259
108 Gly Lys Thr Val Thr Gly Ser Asp Ala.Lys Asp Ser Arg Thr Leu Leu
109             40             45             50
111 cca ctc cgc gcc gtg gga gcc acc atc gca gtg gga cac gct gcg gaa 307
112 Pro Leu Arg Ala Val Gly Ala Thr Ile Ala Val Gly His Ala Ala Glu
113             55             60             65
115 aac ctt gag ctt tcc ggc gaa ctt ccc acc gtc gtg gtg acc tct ttt 355
116 Asn Leu Glu Leu Ser Gly Glu Leu Pro Thr Val Val Val Thr Ser Phe
117 70             75             80             85
119 gcc gcc att ccg caa gac aac ccg gaa ctt gtt cgt gca cgt gaa gaa 403
120 Ala Ala Ile Pro Gln Asp Asn Pro Glu Leu Val Arg Ala Arg Glu Glu
121             90             95             100
123 ggc att ccg gtt att cgt cgc tcc gat ctg ttg ggc gaa ttg ctg gaa 451
124 Gly Ile Pro Val Ile Arg Arg Ser Asp Leu Leu Gly Glu Leu Leu Glu
125             105             110             115
127 ggc tcc acc cag gtc ttg atc gcg ggt acc cac ggt aag acc tcc acc 499
128 Gly Ser Thr Gln Val Leu Ile Ala Gly Thr His Gly Lys Thr Ser Thr
129             120             125             130
131 acc tct atg tct gtg gta gct atg cag gca gcg ggc atg gat cca agc 547
132 Thr Ser Met Ser Val Val Ala Met Gln Ala Ala Gly Met Asp Pro Ser
133             135             140             145
135 ttt gct atc ggc gga cag ctc aac aag gct ggc acc aat gcg cac cat 595
136 Phe Ala Ile Gly Gly Gln Leu Asn Lys Ala Gly Thr Asn Ala His His
137 150             155             160             165

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139	gga	act	ggt	gag	gtc	ttt	atc	gct	gaa	gca	gat	gaa	tct	gac	gca	tcg	
140	Gly	Thr	Gly	Glu	Val	Phe	Ile	Ala	Glu	Ala	Asp	Glu	Ser	Asp	Ala	Ser	
141				170					175						180		
143	ctg	ctg	cgc	tac	aag	cca	aat	gtt	gca	gtg	gtc	acc	aat	gtg	gaa	cca	691
144	Leu	Leu	Arg	Tyr	Lys	Pro	Asn	Val	Ala	Val	Val	Thr	Asn	Val	Glu	Pro	
145				185					190						195		
147	gac	cac	ctg	gac	ttc	ttt	aaa	acc	cct	gaa	gcc	tac	ttc	caa	gtg	ttc	739
148	Asp	His	Leu	Asp	Phe	Phe	Lys	Thr	Pro	Glu	Ala	Tyr	Phe	Gln	Val	Phe	
149				200					205						210		
151	gac	gat	ttc	gca	gga	cgc	atc	acc	ccg	aac	ggc	aag	ctg	gtt	gtg	tgc	787
152	Asp	Asp	Phe	Ala	Gly	Arg	Ile	Thr	Pro	Asn	Gly	Lys	Leu	Val	Val	Cys	
153			215					220				225					
155	ctg	aac	gat	cct	cac	gca	gcg	gag	ctg	ggg	gag	agg	tct	gtc	cgc	aag	835
156	Leu	Asn	Asp	Pro	His	Ala	Ala	Glu	Leu	Gly	Glu	Arg	Ser	Val	Arg	Lys	
157	230					235					240					245	
159	ggt	atc	aag	act	gtt	ggt	tac	ggt	acc	gct	gac	gcc	gta	cag	gca	cac	883
160	Gly	Ile	Lys	Thr	Val	Gly	Tyr	Gly	Thr	Ala	Asp	Ala	Val	Gln	Ala	His	
161					250					255					260		
163	cct	gag	gtt	cca	gcg	atg	gct	acc	atc	gtg	gat	tcc	caa	gtt	gtc	gca	931
164	Pro	Glu	Val	Pro	Ala	Met	Ala	Thr	Ile	Val	Asp	Ser	Gln	Val	Val	Ala	
165				265						270					275		
167	gaa	ggc	acc	cgc	gcc	acc	atc	aac	atc	gat	gga	cag	gaa	gta	tct	gtg	979
168	Glu	Gly	Thr	Arg	Ala	Thr	Ile	Asn	Ile	Asp	Gly	Gln	Glu	Val	Ser	Val	
169			280					285							290		
171	att	ctt	caa	atc	cct	ggt	gat	cac	atg	gta	ctc	aac	ggt	gca	gcc	gcc	1027
172	Ile	Leu	Gln	Ile	Pro	Gly	Asp	His	Met	Val	Leu	Asn	Gly	Ala	Ala	Ala	
173			295					300							305		
175	ctg	ctg	gcc	gga	tac	ctg	gtg	ggt	ggg	gac	gtc	gac	aag	ctt	gtt	gaa	1075
176	Leu	Leu	Ala	Gly	Tyr	Leu	Val	Gly	Gly	Asp	Val	Asp	Lys	Leu	Val	Glu	
177	310					315					320					325	
179	ggc	ttg	tcg	gat	ttc	tcc	ggc	gtg	cga	cgc	cgc	ttt	gag	ttc	cac	ggt	1123
180	Gly	Leu	Ser	Asp	Phe	Ser	Gly	Val	Arg	Arg	Arg	Phe	Glu	Phe	His	Gly	
181					330					335						340	
183	gct	atc	gag	ggc	ggc	aaa	ttt	aat	ggc	gct	gct	att	tat	gat	gat	tac	1171
184	Ala	Ile	Glu	Gly	Lys	Phe	Asn	Gly	Ala	Ala	Ile	Tyr	Asp	Asp	Tyr		
185				345					350						355		
187	gca	cac	cac	cca	acg	gaa	gta	act	gca	gtg	ctc	agc	gct	gcg	cgc	acc	1219
188	Ala	His	His	Pro	Thr	Glu	Val	Thr	Ala	Val	Leu	Ser	Ala	Ala	Arg	Thr	
189				360					365						370		
191	cgg	gtg	aag	gcc	gct	gga	aag	ggc	cgt	gtc	atc	gtc	gcg	ttc	caa	cca	1267
192	Arg	Val	Lys	Ala	Ala	Gly	Lys	Gly	Arg	Val	Ile	Val	Ala	Phe	Gln	Pro	
193			375					380							385		
195	cat	tta	tac	tca	cgc	acc	ata	gaa	ttc	caa	aag	gag	ttc	gcg	ggg	gca	1315
196	His	Leu	Tyr	Ser	Arg	Thr	Ile	Glu	Phe	Gln	Lys	Glu	Phe	Ala	Gly	Ala	
197	390					395					400					405	
199	ctg	tca	ctg	gca	gac	gct	gcc	gtg	gtg	ctt	gag	att	tac	gga	gcg	cgc	1363
200	Leu	Ser	Leu	Ala	Asp	Ala	Ala	Val	Val	Leu	Glu	Ile	Tyr	Gly	Ala	Arg	
201					410					415						420	
203	gaa	caa	ccg	gtg	gat	ggc	gtg	tcc	tcg	gaa	atc	atc	acc	gat	gcg	atg	1411

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204 Glu Gln Pro Val Asp Gly Val Ser Ser Glu Ile Ile Thr Asp Ala Met
205          425          430          435
207 acc att cca gtg gtg tac gaa cct aat ttc tct gca gtc cca gaa cgc 1459
208 Thr Ile Pro Val Val Tyr Glu Pro Asn Phe Ser Ala Val Pro Glu Arg
209          440          445          450
211 att gca gaa atc gca gga cct aat gac atc gtg ctc acc atg ggt gca 1507
212 Ile Ala Glu Ile Ala Gly Pro Asn Asp Ile Val Leu Thr Met Gly Ala
213          455          460          465
215 ggt tcc gtg acc atg ctt gct cca gaa atc ctg gat cag ctg caa aac 1555
216 Gly Ser Val Thr Met Leu Ala Pro Glu Ile Leu Asp Gln Leu Gln Asn
217 470          475          480          485
219 aat taggacgtaa gtgaacaagg cag 1581
220 Asn
224 <210> SEQ ID NO: 2
225 <211> LENGTH: 486
226 <212> TYPE: PRT
227 <213> ORGANISM: Corynebacterium glutamicum
229 <400> SEQUENCE: 2
230 Val Thr Thr Pro His Leu Asp Ser Ala Gln Asp Ile Asp Leu Ser Arg
231 1 5 10 15
233 Val His Leu Ile Gly Ile Gly Gly Ala Gly Met Ser Gly Val Ala Arg
234 20 25 30
236 Ile Leu Leu Ala Arg Gly Lys Thr Val Thr Gly Ser Asp Ala Lys Asp
237 35 40 45
239 Ser Arg Thr Leu Leu Pro Leu Arg Ala Val Gly Ala Thr Ile Ala Val
240 50 55 60
242 Gly His Ala Ala Glu Asn Leu Glu Leu Ser Gly Glu Leu Pro Thr Val
243 65 70 75 80
245 Val Val Thr Ser Phe Ala Ala Ile Pro Gln Asp Asn Pro Glu Leu Val
246 85 90 95
248 Arg Ala Arg Glu Glu Gly Ile Pro Val Ile Arg Arg Ser Asp Leu Leu
249 100 105 110
251 Gly Glu Leu Leu Glu Gly Ser Thr Gln Val Leu Ile Ala Gly Thr His
252 115 120 125
254 Gly Lys Thr Ser Thr Thr Ser Met Ser Val Val Ala Met Gln Ala Ala
255 130 135 140
257 Gly Met Asp Pro Ser Phe Ala Ile Gly Gly Gln Leu Asn Lys Ala Gly
258 145 150 155 160
260 Thr Asn Ala His His Gly Thr Gly Glu Val Phe Ile Ala Glu Ala Asp
261 165 170 175
263 Glu Ser Asp Ala Ser Leu Leu Arg Tyr Lys Pro Asn Val Ala Val Val
264 180 185 190
266 Thr Asn Val Glu Pro Asp His Leu Asp Phe Phe Lys Thr Pro Glu Ala
267 195 200 205
269 Tyr Phe Gln Val Phe Asp Asp Phe Ala Gly Arg Ile Thr Pro Asn Gly
270 210 215 220
272 Lys Leu Val Val Cys Leu Asn Asp Pro His Ala Ala Glu Leu Gly Glu
273 225 230 235 240
275 Arg Ser Val Arg Lys Gly Ile Lys Thr Val Gly Tyr Gly Thr Ala Asp

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```

276          245          250          255
278 Ala Val Gln Ala His Pro Glu Val Pro Ala Met Ala Thr Ile Val Asp
279          260          265          270
281 Ser Gln Val Val Ala Glu Gly Thr Arg Ala Thr Ile Asn Ile Asp Gly
282          275          280          285
284 Gln Glu Val Ser Val Ile Leu Gln Ile Pro Gly Asp His Met Val Leu
285          290          295          300
287 Asn Gly Ala Ala Ala Leu Leu Ala Gly Tyr Leu Val Gly Gly Asp Val
288 305          310          315          320
290 Asp Lys Leu Val Glu Gly Leu Ser Asp Phe Ser Gly Val Arg Arg Arg
291          325          330          335
293 Phe Glu Phe His Gly Ala Ile Glu Gly Gly Lys Phe Asn Gly Ala Ala
294          340          345          350
296 Ile Tyr Asp Asp Tyr Ala His His Pro Thr Glu Val Thr Ala Val Leu
297          355          360          365
299 Ser Ala Ala Arg Thr Arg Val Lys Ala Ala Gly Lys Gly Arg Val Ile
300          370          375          380
302 Val Ala Phe Gln Pro His Leu Tyr Ser Arg Thr Ile Glu Phe Gln Lys
303 385          390          395          400
305 Glu Phe Ala Gly Ala Leu Ser Leu Ala Asp Ala Ala Val Val Leu Glu
306          405          410          415
308 Ile Tyr Gly Ala Arg Glu Gln Pro Val Asp Gly Val Ser Ser Glu Ile
309          420          425          430
311 Ile Thr Asp Ala Met Thr Ile Pro Val Val Tyr Glu Pro Asn Phe Ser
312          435          440          445
314 Ala Val Pro Glu Arg Ile Ala Glu Ile Ala Gly Pro Asn Asp Ile Val
315          450          455          460
317 Leu Thr Met Gly Ala Gly Ser Val Thr Met Leu Ala Pro Glu Ile Leu
318 465          470          475          480
320 Asp Gln Leu Gln Asn Asn
321          485
324 <210> SEQ ID NO: 3
325 <211> LENGTH: 1539
326 <212> TYPE: DNA
327 <213> ORGANISM: Corynebacterium glutamicum
329 <220> FEATURE:
330 <221> NAME/KEY: CDS
331 <222> LOCATION: (101)..(1516)
332 <223> OTHER INFORMATION: RXA02705
334 <400> SEQUENCE: 3
335 cgtgaccatc cgtttctggc tgatcgcat catggctgtg ttggcgggtg tcggtgtgtt 60
337 ttacagcgac tggctccact tagcggaggt ataaataatt atg ggt tct ctg tcc 115
338                                     Met Gly Ser Leu Ser
339                                     1 5
341 cat tta cct cag gcg ctg cag ggc cgt att ctt gtg gcc ggc gct ggt 163
342 His Leu Pro Gln Ala Leu Gln Gly Arg Ile Leu Val Ala Gly Ala Gly
343          10          15          20
345 gtt tcc ggc ctg tcc att gca aag atg ctc agt gag ttg cat tgc gat 211
346 Val Ser Gly Leu Ser Ile Ala Lys Met Leu Ser Glu Leu His Cys Asp

```

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

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Input Set : D:\seqlistcorrected2.txt

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L:29132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:315
L:34115 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:387
L:37091 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:425
L:37134 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:427
L:37136 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:427